

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/830,837A
Source: IFW/b
Date Processed by STIC: 11/10/04

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 11/10/2004

PATENT APPLICATION: US/09/830,837A

TIME: 12:46:06

Input Set : A:\480848.90026.txt

Output Set: N:\CRF4\11102004\I830837A.raw

3 <110> APPLICANT: Institut de Recherches Cliniques de Montreal
 4 DAVIGNON, Jean
 5 LAAKSONEN, Reijo
 6 MARCINKIEWICZ, Mieczyslaw
 7 CHRETIEN, Michel
 8 SEIDAH, Nabil
 10 <120> TITLE OF INVENTION: MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN
 CONVERTASE
 11 WITH A UNIQUE CLEAVAGE SPECIFICITY
 13 <130> FILE REFERENCE: IRCM
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/830,837A
 C--> 16 <141> CURRENT FILING DATE: 2001-10-18
 18 <150> PRIOR APPLICATION NUMBER: CA 2,249,648
 19 <151> PRIOR FILING DATE: 1998-11-04
 21 <160> NUMBER OF SEQ ID NOS: 78
 23 <170> SOFTWARE: PatentIn version 3.2
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 3895
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Rattus sp.
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (418)..(3573)
 35 <400> SEQUENCE: 1
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 40 tcctgctaga tttgggtctg tggtaaaat ggagtttagg actcagtga ctggcccta 180
 42 atgagagaag cccctgtcc aagatggaga agaagcggag aaagaaatga aagcctcttt 240
 44 ttgggccaag ctgtgggtga ccatgggact gaggttttct ttacgttgga caagtctgta 300
 46 ggatggctga tcagtaagg tgcagctttt agcgaaaaca gaaatccact tctgatcaag 360
 48 gaagagccta gtgcaatttg aatttatgca attttatgac catattcact taggacc 417
 50 atg.aag ctc gtc aac atc tgg ctt ctt ctg ctg gtg gtt ttg ctc tgt 465
 51 Met Lys Leu Val Asn Ile Trp Leu Leu Leu Leu Val Val Leu Leu Cys
 52 1 5 10 15
 54 ggg aaa aag cat ctg ggt gac agg ctg ggg aag aaa gct ttt gaa aag 513
 55 Gly Lys Lys His Leu Gly Asp Arg Leu Gly Lys Lys Ala Phe Glu Lys
 56 20 25 30
 58 gcc cca tgc ccc agc tgt tcc cac ctg act ttg aag gtg gaa ttc tcc 561
 59 Ala Pro Cys Pro Ser Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser
 60 35 40 45
 62 tca act gtg gtg gaa tat gaa tat att gtg gct ttc aac gga tac ttc 609
 63 Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
 64 50 55 60
 66 aca gcc aaa gct aga aac tca ttt att tca agt gct cta aaa agc agt 657

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67 Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
68 65 70 75 80
70 gaa gtg gac aac tgg aga ata ata cct cgg aac aac cca tct agt gac 705
71 Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
72 85 90 95
74 tac cct agt gat ttt gag gtg att cag ata aaa gag aag cag aag gcg 753
75 Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
76 100 105 110
78 ggg ctg ctc aca ctt gaa gat cac cca aac atc aag cgg gtg aca ccc 801
79 Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
80 115 120 125
82 cag cgg aaa gtc ttt cgt tcc ctg aag ttt gct gaa tcc gac ccc att 849
83 Gln Arg Lys Val Phe Arg Ser Leu Lys Phe Ala Glu Ser Asp Pro Ile
84 130 135 140
86 gtg ccc tgt aat gag acc cgg tgg agc cag aag tgg cag tca tca cgt 897
87 Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
88 145 150 155 160
90 ccc ctg aaa aga gcc agt ctc tcc ctg ggc tct gga ttc tgg cat gca 945
91 Pro Leu Lys Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
92 165 170 175
94 aca gga agg cat tca agt cga cga ttg ctg aga gcc att cct cgc cag 993
95 Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
96 180 185 190
98 gtt gcc cag aca ttg cag gca gat gtg ctt tgg cag atg gga tac aca 1041
99 Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr
100 195 200 205
102 ggt gct aat gtc agg gtt gcc gtt ttt gat act ggg ctc agt gag aag 1089
103 Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys
104 210 215 220
106 cat cca cat ttc aag aat gtg aag gaa aga acc aac tgg acc aat gag 1137
107 His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
108 225 230 235 240
110 cgg acc ctg gac gat ggg ctg ggc cat ggc aca ttc gtt gca ggt gtg 1185
111 Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
112 245 250 255
114 att gcc agc atg aga gag tgc caa gga ttt gcc cca gat gca gag ctg 1233
115 Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu
116 260 265 270
118 cac atc ttc agg gtc ttt acc aac aat cag gtg tct tac acg tct tgg 1281
119 His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp
120 275 280 285
122 ttt ttg gat gcc ttc aac tat gcc atc cta aag aag atg gac gtt ctg 1329
123 Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp Val Leu
124 290 295 300
126 aac ctt agc atc ggt ggg cct gac ttc atg gat cac ccc ttt gtt gac 1377
127 Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp
128 305 310 315 320
130 aag gta tgg gaa tta aca gcg aac aat gta atc atg gtt tct gct att 1425
131 Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile

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Input Set : A:\480848.90026.txt

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132		325		330		335		
134	ggc aat gat gga cct ctc tat ggc act ctg aat aac cct gct gat cag							1473
135	Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln							
136		340		345		350		
138	atg gat gtg att gga gtg ggt ggc att gac ttt gaa gac aac atc gcc							1521
139	Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala							
140		355		360		365		
142	cgc ttc tct tcc agg gga atg act acc tgg gaa cta ccg gga ggc tat							1569
143	Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr							
144		370		375		380		
146	ggt cgt gtg aag cct gac att gtc acc tat ggt gct gga gtg cgg ggt							1617
147	Gly Arg Val Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly							
148	385		390		395		400	
150	tct ggt gtg aaa ggg ggc tgc cgt gca ctc tca ggg acc agt gtc gcc							1665
151	Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala							
152		405		410		415		
154	tcc cca gtg gtt gct ggg gct gtc acc ttg tta gta agc aca gta cag							1713
155	Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln							
156		420		425		430		
158	aag cgg gag cta gtg aat cct gcc agt gtg aag caa gct ttg ata gca							1761
159	Lys Arg Glu Leu Val Asn Pro Ala Ser Val Lys Gln Ala Leu Ile Ala							
160		435		440		445		
162	tca gcc cgg aga ctt cct ggt gtc aac atg ttt gag caa ggc cat ggc							1809
163	Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly							
164		450		455		460		
166	aag ttg gat cta ctg cga gcc tat cag atc ctc agc agc tat aaa ccg							1857
167	Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Ser Ser Tyr Lys Pro							
168	465		470		475		480	
170	cag gcg agc ctg agt cct agc tac atc gac ctg act gag tgt ccc tac							1905
171	Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr							
172		485		490		495		
174	atg tgg ccc tac tgc tcc cag ccc atc tac tat gga gga atg cca aca							1953
175	Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr							
176		500		505		510		
178	att gtt aat gtc acc atc ctc aat ggc atg gga gtt aca gga aga att							2001
179	Ile Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile							
180		515		520		525		
182	gtg gat aag cct gag tgg cga ccc tat tta cca cag aat gga gac aac							2049
183	Val Asp Lys Pro Glu Trp Arg Pro Tyr Leu Pro Gln Asn Gly Asp Asn							
184		530		535		540		
186	att gaa gtg gcc ttc tcc tac tcc tca gtg ttg tgg cct tgg tca ggt							2097
187	Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly							
188	545		550		555		560	
190	tac ctt gcc atc tcc att tct gtg acc aag aag gca gct tcc tgg gaa							2145
191	Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu							
192		565		570		575		
194	ggc atc gcg cag ggc cac atc atg atc aca gtg gct tcc cca gca gag							2193
195	Gly Ile Ala Gln Gly His Ile Met Ile Thr Val Ala Ser Pro Ala Glu							
196		580		585		590		

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198	acg	gaa	tta	aaa	aat	ggt	gcc	gag	cat	act	tcc	aca	gtg	aag	ctg	ccc	2241
199	Thr	Glu	Leu	Lys	Asn	Gly	Ala	Glu	His	Thr	Ser	Thr	Val	Lys	Leu	Pro	
200			595				600					605					
202	atc	aag	gtg	aag	atc	att	ccc	acc	cct	cct	cgg	agc	aag	aga	gtc	ctc	2289
203	Ile	Lys	Val	Lys	Ile	Ile	Pro	Thr	Pro	Pro	Arg	Ser	Lys	Arg	Val	Leu	
204		610					615					620					
206	tgg	gac	cag	tac	cac	aac	ctc	cgc	tac	cca	ccc	ggc	tac	ttc	ccc	agg	2337
207	Trp	Asp	Gln	Tyr	His	Asn	Leu	Arg	Tyr	Pro	Pro	Gly	Tyr	Phe	Pro	Arg	
208	625					630					635					640	
210	gac	aac	ttg	cgg	atg	aag	aat	gat	cct	tta	gac	tgg	aat	ggc	gac	cac	2385
211	Asp	Asn	Leu	Arg	Met	Lys	Asn	Asp	Pro	Leu	Asp	Trp	Asn	Gly	Asp	His	
212					645					650					655		
214	gtc	cac	acc	aac	ttc	agg	gac	atg	tac	cag	cat	ctg	cgc	agc	atg	ggc	2433
215	Val	His	Thr	Asn	Phe	Arg	Asp	Met	Tyr	Gln	His	Leu	Arg	Ser	Met	Gly	
216			660						665					670			
218	tac	ttt	gtg	gag	gtg	ctt	ggt	gcc	cca	ttc	aca	tgc	ttt	gac	gcc	acg	2481
219	Tyr	Phe	Val	Glu	Val	Leu	Gly	Ala	Pro	Phe	Thr	Cys	Phe	Asp	Ala	Thr	
220			675					680					685	o			
222	cag	tac	ggc	act	ctg	ctt	atg	gtg	gac	agt	gag	gaa	gag	tac	ttc	cct	2529
223	Gln	Tyr	Gly	Thr	Leu	Leu	Met	Val	Asp	Ser	Glu	Glu	Glu	Tyr	Phe	Pro	
224		690					695				700						
226	gag	gag	att	gct	aag	ctg	agg	agg	gac	gtg	gac	aat	ggc	ctt	tcc	ctt	2577
227	Glu	Glu	Ile	Ala	Lys	Leu	Arg	Arg	Asp	Val	Asp	Asn	Gly	Leu	Ser	Leu	
228	705				710					715					720		
230	gtc	gtc	ttc	agt	gac	tgg	tac	aac	act	tct	gtt	atg	aga	aaa	gtg	aag	2625
231	Val	Val	Phe	Ser	Asp	Trp	Tyr	Asn	Thr	Ser	Val	Met	Arg	Lys	Val	Lys	
232				725					730					735			
234	ttt	tac	gat	gaa	aac	aca	agg	cag	tgg	tgg	atg	cca	gat	act	gga	gga	2673
235	Phe	Tyr	Asp	Glu	Asn	Thr	Arg	Gln	Trp	Trp	Met	Pro	Asp	Thr	Gly	Gly	
236			740					745				750					
238	gcc	aac	gtc	cca	gct	cta	aac	gag	ctg	ctg	tct	gtg	tgg	aac	atg	ggg	2721
239	Ala	Asn	Val	Pro	Ala	Leu	Asn	Glu	Leu	Leu	Ser	Val	Trp	Asn	Met	Gly	
240			755					760				765					
242	ttc	agt	gac	ggc	ctg	tat	gaa	ggg	gag	ttt	gcc	ctg	gca	aac	cac	gac	2769
243	Phe	Ser	Asp	Gly	Leu	Tyr	Glu	Gly	Glu	Phe	Ala	Leu	Ala	Asn	His	Asp	
244		770					775				780						
246	atg	tac	tat	gca	tgc	ggg	tgc	agc	att	gcc	agg	ttt	cca	gaa	gat	ggt	2817
247	Met	Tyr	Tyr	Ala	Ser	Gly	Cys	Ser	Ile	Ala	Arg	Phe	Pro	Glu	Asp	Gly	
248	785				790				795						800		
250	gtg	gtg	atc	aca	cag	act	ttc	aag	gac	caa	gga	ttg	gaa	gtc	tta	aaa	2865
251	Val	Val	Ile	Thr	Gln	Thr	Phe	Lys	Asp	Gln	Gly	Leu	Glu	Val	Leu	Lys	
252				805					810					815			
254	caa	gag	aca	gca	gtt	gtc	gac	aat	gtc	ccc	att	ctg	ggg	cta	tat	cag	2913
255	Gln	Glu	Thr	Ala	Val	Val	Asp	Asn	Val	Pro	Ile	Leu	Gly	Leu	Tyr	Gln	
256			820						825				830				
258	att	cca	gct	gaa	ggt	gga	ggc	cgg	att	gtg	ctg	tat	gga	gac	tcc	aac	2961
259	Ile	Pro	Ala	Glu	Gly	Gly	Gly	Arg	Ile	Val	Leu	Tyr	Gly	Asp	Ser	Asn	
260			835					840					845				
262	tgc	ttg	gat	gac	agt	cac	aga	cag	aag	gac	tgc	ttt	tgg	ctt	ctg	gat	3009

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263 Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp
264      850                      855                      860
266 gca ctc ctt cag tac aca tcc tat ggt gtg acc cct ccc agc ctc agc      3057
267 Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser
268 865                      870                      875                      880
270 cat tca ggg aac cgg cag cgc cca ccc agc ggg gct ggc ttg gcc cct      3105
271 His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Leu Ala Pro
272                      885                      890                      895
274 cct gaa agg atg gaa gga aac cac ctt cat cgc tac tcc aaa gtt ctt      3153
275 Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
276      900                      905                      910
278 gag gcc cac ttg gga gac ccg aaa cct cgg ccc ctt cca gcc tgt cca      3201
279 Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
280      915                      920                      925
282 cac ttg tcg tgg gcc aag cca cag cct ttg aat gag acg gca ccc agt      3249
283 His Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
284      930                      935                      940
286 aat ctt tgg aaa cac cag aag ctg ctc tcc att gac ctg gac aaa gta      3297
287 Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val
288 945                      950                      955                      960
290 gtg tta ccc aac ttt cgc tca aat cgc cct caa gtg aga cct ttg tcc      3345
291 Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser
292      965                      970                      975
294 cct gga gaa agt ggt gcc tgg gac att cct gga ggg atc atg cct ggc      3393
295 Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly
296      980                      985                      990
298 cgc tac aac cag gaa gta ggc cag acc atc cct gtt ttt gcc ttc ctt      3441
299 Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu
300      995                      1000                      1005
302 gga gcc atg gtg gcc ctg gcc ttc ttc gtg gta cag atc agt aag      3486
303 Gly Ala Met Val Ala Leu Ala Phe Phe Val Val Gln Ile Ser Lys
304      1010                      1015                      1020
306 gcc aag agc cgg ccg aag cgg agg agg ccc agg gca aag cgt cca      3531
307 Ala Lys Ser Arg Pro Lys Arg Arg Arg Pro Arg Ala Lys Arg Pro
308      1025                      1030                      1035
310 caa ctt gca cag cag gcc cac cct gca agg acc ccg tca gtg      3573
311 Gln Leu Ala Gln Gln Ala His Pro Ala Arg Thr Pro Ser Val
312      1040                      1045                      1050
314 tgatcatcac agtggccaga cacagaagct gacaagcttt gaacccctct ggtggccaca      3633
316 cagcatcaga gagcatcctg ggaagtgcct gtttccaagg agccctatct ctggattgtg      3693
318 gctggcttag tgtgttctgc ccagacgtct atgaggtaca tcctgcagtg cctcactgtg      3753
320 tttggctctg gccgaagggtg ccagtagct cagcctccgg tggcatcagg ccagtgaca      3813
322 gtgcacaaa gacacagagc ctggaagggtg tgtcgggaca tactttctac ataatgctac      3873
324 aaccctgacc aagcgaagac at      3895
327 <210> SEQ ID NO: 2
328 <211> LENGTH: 1052
329 <212> TYPE: PRT
330 <213> ORGANISM: Rattus sp.
332 <400> SEQUENCE: 2

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/10/2004
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Release Note:

Sequence of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> or <223> fields of each sequence which presents at least one n or Xaa.

eq#:7; Xaa Pos. 2,3,4,5,6,7
 eq#:8; Xaa Pos. 2,3,4,5,6,7
 eq#:9; Xaa Pos. 2,3,4,5,6,7,8
 eq#:10; Xaa Pos. 2,3,4,5,6,7,8
 eq#:11; Xaa Pos. 2,3,4,5,6,7,8,9
 eq#:12; Xaa Pos. 2,3,4,5,6,7,8,9
 eq#:14; Xaa Pos. 1,13
 eq#:15; N Pos. 3,9,12,18,21
 eq#:16; N Pos. 3,6,9,12,15,18,21,24,29
 eq#:17; Xaa Pos. 5,6
 eq#:18; Xaa Pos. 4,6,8,10
 eq#:46; Xaa Pos. 1,13
 eq#:47; Xaa Pos. 1,11
 eq#:74; Xaa Pos. 1,13
 eq#:75; Xaa Pos. 1,11
 eq#:76; Xaa Pos. 1,14

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
 per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

eq#:77,78

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0

L:1794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0

L:1814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0

L:1834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0

L:1854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:1874 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

L:1913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0

L:1952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

L:2010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0

L:2029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0

L:2064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0

L:2402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0

L:2427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0

L:2741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0

L:2766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0

L:2791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0